SEQUENCE LISTING TABLE

The sequences referred to in the specification above are provided in the following table.

SEQ ID NO: 1

     5'-CATTCTAGAACCTCGACAAGCTTGAGATCACAGTTCTCTCTAC-3'

SEQ ID NO: 2

     5'-CAGCAGGCTGGGCCACGTGCATTGCGGAGTGGACACCTGTGGAGAG-3'

SEQ ID NO: 3

     5'-CTCTCCACAGGTGTCCACTCCGCAATGCACGTGGCCCAGCCTGCTG-3'

SEQ ID NO: 4

     5'-TGTGTGTGGAATTCTCATTACTGATCAGAATCTGGGCACGGTTCTG-3'

SEQ ID NO: 5

     5'-GCATTTTAAGCTTTTTCCTGATCAGGAGCCCAAATCTTCT

     GACAAAACTCACACATCTCCACCGTCTCCAGGTAAGCC-3'

SEQ ID NO: 6

     5'TAATACGACTCACTATAGGG-3'

SEQ ID NO: 7

     5'GAGCATTTTCCTGATCAGGAGTCCAAATATGGTCCCCCACCCC

     ATCATCCCCAGGTAAGCCAACCC-3'

SEQ ID NO: 8

     5'GCAGAGGAATTCGAGCTCGGTACCCGGGGATCCCCAGTGTGGGG

     ACAGTGGGACCCGCTCTGCCTCCC-3'

SEQ ID NO: 9

     5'-GGGTTTTGGGGGGAAGAGGAAGACTGACGGTGCCCCCTCGGCTT

     CAGGTGCTGAGGAAG-3'

SEQ ID NO: 10   5'-CATCTCTTCCTCAGCACCTGAAGCCGAGGGGGCACCGTCAGTCT

     TCCTCTTCCCCC-3'

SEQ ID NO:11   5'-CGCACGTGACCTCAGGGGTCCGGGAGATCATGAGAGTGTCCTTG
GGTTTTGGGGGGAACAGGAAGACTGATGGTGCCCCCTCGAACTCAG GTGCTGAGG-3'

SEQ ID NO: 12   5'-CCTCAGCACCTGAGTTCGAGGGGGCACCATCAGTCTTCCTGTTCCC
CCCAAAACCCAAGGACACTCTCATGATCTCCCGGACCCCTGAGGTCA CGTGCG-3'

SEQ ID NO: 13
5'CATTCGCTTACCTCGACAAGCTTGAGATCACAGTTCTCTCTAC-3'

SEQ ID NO: 14
5'-GGAGTGGACACCTGTGGAGAG-3'

SEQ ID NO: 15
5'-CTCCACAGGTGTCCACTCCGCAATGCACGTGGCCCAGCC-3'

SEQ ID NO: 16
5'GAGGTTGTAAGGACTCACCTGAAATCTGGGCTCCGTTGC-3'

SEQ ID NO: 17
5'-GCAACGGAGCCCAGATTTCAGGTGAGTCCTTACAACCTC-3'

SEQ ID NO: 18
5'-GGCTAGATATCTCTAGACTATAAATCTCTGGCCATGAAG-3'

SEQ ID NO: 19
5'-GGCACTAGGTCGACTCTAGAAACTGAGGAAGCAAAGTTTAAATTCTAC
TCACGTTTAATCTGGGCTCCGTTGC-3'

SEQ ID NO: 20
5'GCAGAGAGACATATGGCAATGCACGTGGCCCAGCCTGCTGTGG-3'

SEQ ID NO: 21
5'-GCAGAGAGAGGATCCTCAGTCAGTTAGTCAGAATCTGGGCACGGTT
CTGG-3'

SEQ ID NO: 22
5'-GGCACTAGTCATGAAATACCTATTGCCTACGGCAGCCGCTGGA
TTGTTATTACTCGCTGCCCAACCAGCGATGGCCGCAGCAA

TGCACGTGGCCCAGCCTGCTGTGG-3'

SEQ ID NO: 23

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  1 CATTCGCTTA CCTCGAGAAG CTTGAGATCA CAGTTCTCTC TACAGTTACT

 51 GAGCACACAG GACCTCACCA TGGGATGGAG CTGTATCATC CTCTTCTTGG

101 TAGCAACAGC TACAGGTAAG GGGCTCACAG TAGCAGGCTT GAGGTCTGGA

151 CATATATATG GGTGACAATG ACATCCACTT TGCCTTTCTC TCCACAGGTG

201 TCCACTCCGC AATGCACGTG GCCCAGCCTG CTGTGGTACT GGCCAGCAGC

251 CGAGGCATCG CCAGCTTTGT GTGTGAGTAT GCATCTCCAG GCAAAGCCAC

301 TGAGGTCCGG GTGACAGTGC TTCGGCAGGC TGACAGCCAG GTGACTGAAG

351 TCTGTGCGGC AACCTACATG ATGGGGAATG AGTTGACCTT CCTAGATGAT

401 TCCATCTGCA CGGGCACCTC CAGTGGAAAT CAAGTGAACC TCACTATCCA

451 AGGACTGAGG GCCATGGACA CGGGACTCTA CATCTGCAAG GTGGAGCTCA

501 TGTACCCACC GCCATACTAC CTGGGCATAG GCAACGGAAC CCAGATTTAT

551 GTAATTGATC CAGAACCGTG CCCAGATTCT GATCAGGAGC CCAAATCTTC

601 TGACAAAACT CACACATCTC CACCGTCTCC AGGTAAGCCA GCCCAGGCCT

651 CGCCCTCCAG CTCAAGGCGG GACAGGTGCC CTAGAGTAGC CTGCATCCAG

701 GGACAGGCCC CAGCCGGGTG CTGACACGTC CACCTCCATC TCTTCCTCAG

751 CACCTGAAGC CGAGGGGGCA CCGTCAGTCT TCCTCTTCCC CCCAAAACCC

801 AAGGACACCC TCATGATCTC CCGGACCCCT GAGGTCACAT GCGTGGTGGT

851 GGACGTGAGC CACGAAGACC CTGAGGTCAA GTTCAACTGG TACGTGGACG

901 GCGTGGAGGT GCATAATGCC AAGACAAAGC CGCGGGAGGA GCAGTACAAC

951 AGCACGTACC GGGTGGTCAG CGTCCTCACC GTCCTGCACC AGGACTGGCT

1001 GAATGGCAAG GAGTACAAGT GCAAGGTCTC CAACAAAGCC CTCCCAGCCC

1051 CCATCGAGAA AACCATCTCC AAAGCCAAAG GTGGGACCCG TGGGGTGCGA

1101 GGGCCACATG GACAGAGGCC GGCTCGGCCC ACCCTCTGCC CTGAGAGTGA

1151 CCGCTGTACC AACCTCTGTC CTACAGGGCA GCCCCGAGAA CCACAGGTGT

1201 ACACCCTGCC CCCATCCCGG GATGAGCTGA CCAAGAACCA GGTCAGCCTG

1251 ACCTGCCTGG TCAAAGGCTT CTATCCCAGC GACATCGCCG TGGAGTGGGA
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1301  GAGCAATGGG CAGCCGGAGA ACAACTACAA GACCACGCCT CCCGTGCTGG

1351  ACTCCGACGG CTCCTTCTTC CTCTACAGCA AGCTCACCGT GGACAAGAGC

1401  AGGTGGCAGC AGGGGAACGT CTTCTCATGC TCCGTGATGC ATGAGGCTCT

1451  GCACAACCAC TACACGCAGA AGAGCCTCTC CCTGTCTCCG GGTAAATGAG

1501  TGCGACGGCC GGCAAGCCCC GCTCCCCGGG CTCTCGCGGT CGCACGAGGA

1551  TGCTTGGCAC GTACCCCCTG TACATACTTC CCGGGCGCCC AGCATGGAAA

1601  TAAAGCACCC AGCGCTGCCC TGGGCCCCTG CGAGACTGTG ATGGTTCTTT

1651  CCACGGGTCA GGCCGAGTCT GAGGCCTGAG TGGCATGAGG GAGGCAGAGC

1701  GGGTC
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SEQ ID NO:24

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  1  MGWSCIILFL VATATGVHSA MHVAQPAVVL ASSRGIASFV CEYASPGKAT

 51  EVRVTVLRQA DSQVTEVCAA TYMMGNELTF LDDSICTGTS SGNQVNLTIQ

101  GLRAMDTGLY ICKVELMYPP PYYLGIGNGT QIYVIDPEPC PDSDQEPKSS

151  DKTHTSPPSP APEAEGAPSV FLFPPKPKDT LMISRTPEVT CVVVDVSHED

201  PEVKFNWYVD GVEVHNAKTK PREEQYNSTY RVVSVLTVLH QDWLNGKEYK

251  CKVSNKALPA PIEKTISKAK GQPREPQVYT LPPSRDELTK NQVSLTCLVK

301  GFYPSDIAVE WESNGQPENN YKTTPPVLDS DGSFFLYSKL TVDKSRWQQG

351  NVFSCSVMHE ALHNHYTQKS LSLSPGK*
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SEQ ID NO: 25

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  1  CATTCGCTTA CCTCGAGAAG CTTGAGATCA CAGTTCTCTC TACAGTTACT

 51  GAGCACACAG GACCTCACCA TGGGATGGAG CTGTATCATC CTCTTCTTGG

101  TAGCAACAGC TACAGGTAAG GGGCTCACAG TAGCAGGCTT GAGGTCTGGA

151  CATATATATG GGTGACAATG ACATCCACTT TGCCTTTCTC TCCACAGGTG

201  TCCACTCCGC AATGCACGTG GCCCAGCCTG CTGTGGTACT GGCCAGCAGC

251  CGAGGCATCG CCAGCTTTGT GTGTGAGTAT GCATCTCCAG GCAAAGCCAC

301  TGAGGTCCGG GTGACAGTGC TTCGGCAGGC TGACAGCCAG GTGACTGAAG

351  TCTGTGCGGC AACCTACATG ATGGGGAATG AGTTGACCTT CCTAGATGAT
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401  TCCATCTGCA CGGGCACCTC CAGTGGAAAT CAAGTGAACC TCACTATCCA

451  AGGACTGAGG GCCATGGACA CGGGACTCTA CATCTGCAAG GTGGAGCTCA

501  TGTACCCACC GCCATACTAC CTGGGCATAG GCAACGGAAC CCAGATTTAT

551  GTAATTGATC CAGAACCGTG CCCAGATTCT GATCAGGAGT CCAAATATGG

601  TCCCCCATCC CCATCATCCC CAGGTAAGCC AACCCAGGCC TCGCCCTCCA

651  GCTCAAGGCG GGACAGGTGC CCTAGAGTAG CCTGCATCCA GGGACAGGCC

701  CCAGCCGGGT GCTGACGCAT CCACCTCCAT CTCTTCCTCA GCACCTGAGT

751  TCCTGGGGGG ACCATCAGTC TTCCTGTTCC CCCCAAAACC CAAGGACACT

801  CTCATGATCT CCCGGACCCC TGAGGTCACG TGCGTGGTGG TGGACGTGAG

851  CCAGGAAGAC CCCGAGGTCC AGTTCAACTG GTACGTGGAT GGCGTGGAGG

901  TGCATAATGC CAAGACAAAG CCGCGGGAGG AGCAGTTCAA CAGCACGTAC

951  CGTGTGGTCA GCGTCCTCAC CGTCCTGCAC CAGGACTGGC TGAACGGCAA

1001 GGAGTACAAG TGCAAGGTCT CCAACAAAGG CCTCCCGTCC TCCATCGAGA

1051 AAACCATCTC CAAAGCCAAA GGTGGGACCC ACGGGGTGCG AGGGCCACAC

1101 GGACAGAGGC CAGCTCGGCC CACCCTCTGC CCTGGGAGTG ACCGCTGTGC

1151 CAACCTCTGT CCCTACAGGG CAGCCCCGAG AGCCACAGGT GTACACCCTG

1201 CCCCCATCCC AGGAGGAGAT GACCAAGAAC CAGGTCAGCC TGACCTGCCT

1251 GGTCAAAGGC TTCTACCCCA GCGACATCGC CGTGGAGTGG GAGAGCAATG

1301 GGCAGCCGGA GAACAACTAC AAGACCACGC CTCCCGTGCT GGACTCCGAC

1351 GGCTCCTTCT TCCTCTACAG CAGGCTAACC GTGGACAAGA GCAGGTGGCA

1401 GGAGGGGAAT GTCTTCTCAT GCTCCGTGAT GCATGAGGCT CTGCACAACC

1451 ACTACACACA GAAGAGCCTC TCCCTGTCTC TGGGTAAATG AGTGCCAGGG

1501 CCGGCAAGCC CCCGCTCCCC GGGCTCTCGG GGTCGCGCGA GGATGCTTGG

1551 CACGTACCCC GTCTACATAC TTCCCAGGCA CCCAGCATGG AAATAAAGCA

1601 CCCACCACTG CCCTGGGCCC CTGTGAGACT GTGATGGTTC TTTCCACGGG

1651 TCAGGCCGAG TCTGAGGCCT GAGTGACATG AGGGAGGCAG AGCGGTCCCA

1701 CTGTCCCCAC ACTGGGGATC CCCGGGTACC GAGCTCGATT CCTCTGC .
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SEQ ID NO:26

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  1  MGWSCIILFL VATATGVHSA MHVAQPAVVL ASSRGIASFV CEYASPGKAT

 51  EVRVTVLRQA DSQVTEVCAA TYMMGNELTF LDDSICTGTS SGNQVNLTIQ

101  GLRAMDTGLY ICKVELMYPP PYYLGIGNGT QIYVIDPEPC PDSDQESKYG

151  PPSPSSPAPE FEGAPSVFLF PPKPKDTLMI SRTPEVTCVV VDVSQEDPEV

201  QFNWYVDGVE VHNAKTKPRE EQFNSTYRVV SVLTVLHQDW LNGKEYKCKV

251  SNKGLPSSIE KTISKAKGQP REPQVYTLPP SQEEMTKNQV SLTCLVKGFY

301  PSDIAVEWES NGQPENNYKT TPPVLDSDGS FFLYSRLTVD KSRWQEGNVF

351  SCSVMHEALH NHYTQKSLSL SLGK*
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SEQ ID NO: 27

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  1  CATTCGCTTA CCTCGAGAAG CTTGAGATCA CAGTTCTCTC TACAGTTACT

 51  GAGCACACAG GACCTCACCA TGGGATGGAG CTGTATCATC CTCTTCTTGG

101  TAGCAACAGC TACAGGTAAG GGGCTCACAG TAGCAGGCTT GAGGTCTGGA

151  CATATATATG GGTGACAATG ACATCCACTT TGCCTTTCTC TCCACAGGTG

201  TCCACTCCGC AATGCACGTG GCCCAGCCTG CTGTGGTACT GGCCAGCAGC

251  CGAGGCATCG CCAGCTTTGT GTGTGAGTAT GCATCTCCAG GCAAAGCCAC

301  TGAGGTCCGG GTGACAGTGC TTCGGCAGGC TGACAGCCAG GTGACTGAAG

351  TCTGTGCGGC AACCTACATG ATGGGGAATG AGTTGACCTT CCTAGATGAT

401  TCCATCTGCA CGGGCACCTC CAGTGGAAAT CAAGTGAACC TCACTATCCA

451  AGGACTGAGG GCCATGGACA CGGGACTCTA CATCTGCAAG GTGGAGCTCA

501  TGTACCCACC GCCATACTAC CTGGGCATAG GCAACGGAAC CCAGATTTAT

551  GTAATTGATC CAGAACCGTG CCCAGATTCT GATCAGGAGT CCAAATATGG

601  TCCCCCATCC CCATCATCCC CAGGTAAGCC AACCCAGGCC TCGCCCTCCA

651  GCTCAAGGCG GACAGGTGC CCTAGAGTAG CCTGCATCCA GGGACAGGCC

701  CCAGCCGGGT GCTGACGCAT CCACCTCCAT CTCTTCCTCA GCACCTGAGT

751  TCGAGGGGGC ACCATCAGTC TTCCTGTTCC CCCCAAAACC CAAGGACACT

801  CTCATGATCT CCCGGACCCC TGAGGTCACG TGCGTGGTGG TGGACGTGAG
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851   CCAGGAAGAC CCCGAGGTCC AGTTCAACTG GTACGTGGAT GGCGTGGAGG

901   TGCATAATGC CAAGACAAAG CCGCGGGAGG AGCAGTTCAA CAGCACGTAC

951   CGTGTGGTCA GCGTCCTCAC CGTCCTGCAC CAGGACTGGC TGAACGGCAA

1001  GGAGTACAAG TGCAAGGTCT CCAACAAAGG CCTCCCGTCC TCCATCGAGA

1051  AAACCATCTC CAAAGCCAAA GGTGGGACCC ACGGGGTGCG AGGGCCACAC

1101  GGACAGAGGC CAGCTCGGCC CACCCTCTGC CCTGGGAGTG ACCGCTGTGC

1151  CAACCTCTGT CCCTACAGGG CAGCCCCGAG AGCCACAGGT GTACACCCTG

1201  CCCCCATCCC AGGAGGAGAT GACCAAGAAC CAGGTCAGCC TGACCTGCCT

1251  GGTCAAAGGC TTCTACCCCA GCGACATCGC CGTGGAGTGG GAGAGCAATG

1301  GGCAGCCGGA GAACAACTAC AAGACCACGC CTCCCGTGCT GGACTCCGAC

1351  GGCTCCTTCT TCCTCTACAG CAGGCTAACC GTGGACAAGA GCAGGTGGCA

1401  GGAGGGGAAT GTCTTCTCAT GCTCCGTGAT GCATGAGGCT CTGCACAACC

1451  ACTACACACA GAAGAGCCTC TCCCTGTCTC TGGGTAAATG AGTGCCAGGG

1501  CCGGCAAGCC CCCGCTCCCC GGGCTCTCGG GGTCGCGCGA GGATGCTTGG

1551  CACGTACCCC GTCTACATAC TTCCCAGGCA CCCAGCATGG AAATAAAGCA

1601  CCCACCACTG CCCTGGGCCC CTGTGAGACT GTGATGGTTC TTTCCACGGG

1651  TCAGGCCGAG TCTGAGGCCT GAGTGACATG AGGGAGGCAG AGCGGTCCCA

1701  CTGTCCCCAC ACTGGGGATC CCGGGTACC GAGCTCGATT CCTCTGC
```

SEQ ID NO:28

```
1     MGWSCIILFL VATATGVHSA MHVAQPAVVL ASSRGIASFV CEYASPGKAT

51    EVRVTVLRQA DSQVTEVCAA TYMMGNELTF LDDSICTGTS SGNQVNLTIQ

101   GLRAMDTGLY ICKVELMYPP PYYLGIGNGT QIYVIDPEPC PDSDQESKYG

151   PPSPSSPAPE FEGAPSVFLF PPKPKDTLMI SRTPEVTCVV VDVSQEDPEV

201   QFNWYVDGVE VHNAKTKPRE EQFNSTYRVV SVLTVLHQDW LNGKEYKCKV

251   SNKGLPSSIE KTISKAKGQP REPQVYTLPP SQEEMTKNQV SLTCLVKGFY

301   PSDIAVEWES NGQPENNYKT TPPVLDSDGS FFLYSRLTVD KSRWQEGNVF

351   SCSVMHEALH NHYTQKSLSL SLGK*
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SEQ ID NO: 29

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   1   CATTCGCTTA CCTCGAGAAG CTTGAGATCA CAGTTCTCTC TACAGTTACT
  51   GAGCACACAG GACCTCACCA TGGGATGGAG CTGTATCATC CTCTTCTTGG
 101   TAGCAACAGC TACAGGTAAG GGGCTCACAG TAGCAGGCTT GAGGTCTGGA
 151   CATATATATG GGTGACAATG ACATCCACTT TGCCTTTCTC TCCACAGGTG
 201   TCCACTCCGC AATGCACGTG GCCCAGCCTG CTGTGGTACT GGCCAGCAGC
 251   CGAGGCATCG CCAGCTTTGT GTGTGAGTAT GCATCTCCAG GCAAAGCCAC
 301   TGAGGTCCGG GTGACAGTGC TTCGGCAGGC TGACAGCCAG GTGACTGAAG
 351   TCTGTGCGGC AACCTACATG ATGGGGAATG AGTTGACCTT CCTAGATGAT
 401   TCCATCTGCA CGGGCACCTC CAGTGGAAAT CAAGTGAACC TCACTATCCA
 451   AGGACTGAGG GCCATGGACA CGGGACTCTA CATCTGCAAG GTGGAGCTCA
 501   TGTACCCACC GCCATACTAC CTGGGCATAG CAACGGAGC CCAGATTTCA
 551   GGTGAGTCCT TACAACCTCT CTCTTCTATT CAGCTTAAAT AGATTTTACT
 601   GCATTTGTTG GGGGGGAAAT GTGTGTATCT GAATTTCAGG TCATGAAGGA
 651   CTAGGGACAC CTTGGGAGTC AGAAAGGGTC ATTGGGAGCC CGGGCTGATG
 701   CAGACAGACA TCCTCAGCTC CCAGACTTCA TGGCCAGAGA TTTATAGTCT
 751   AGAGGATCCC CAGCTTTCTG GGGCAGGCCA GGCCTGACCT TGGCTTTGGG
 801   GCAGGGAGGG GGCTAAGGTG AGGCAGGTGG CGCCAGCAGG TGCACACCCA
 851   ATGCCCATGA GCCCAGACAC TGGACGCTGA ACCTCGCGGA CAGTTAAGAA
 901   CCCAGGGGCC TCTGCGCCTG GGCCCAGCTC TGTCCCACAC CGCGGTCACA
 951   TGGCACCACC TCTCTTGCAG CCTCCACCAA GGGCCCATCG GTCTTCCCCC
1001   TGGCACCCTC CTCCAAGAGC ACCTCTGGGG CACAGCGGC CCTGGGCTGC
1051   CTGGTCAAGG ACTACTTCCC CGAACCGGTG ACGGTGTCGT GGAACTCAGG
1101   CGCCCTGACC AGCGGCGTGC ACACCTTCCC GGCTGTCCTA CAGTCCTCAG
1151   GACTCTACTC CCTCAGCAGC GTGGTGACCG TGCCCTCCAG CAGCTTGGGC
1201   ACCCAGACCT ACATCTGCAA CGTGAATCAC AAGCCCAGCA ACACCAAGGT
1251   GGACAAGAAA GTTGGTGAGA GGCCAGCACA GGGAGGGAGG GTGTCTGCTG
1301   GAAGCAGGCT CAGCGCTCCT GCCTGGACGC ATCCCGGCTA TGCAGCCCCA
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1351   GTCCAGGGCA GCAAGGCAGG CCCCGTCTGC CTCTTCACCC GGAGCCTCTG

1401   CCCGCCCCAC TCATGCTCAG GGAGAGGGTC TTCTGGCTTT TTCCCAGGCT

1451   CTGGGCAGGC ACAGGCTAGG TGCCCCTAAC CCAGGCCCTG CACACAAAGG

1501   GGCAGGTGCT GGGCTCAGAC CTGCCAAGAG CCATATCCGG GAGGACCCTG

1551   CCCCTGACCT AAGCCCACCC CAAAGGCCAA ACTCTCCACT CCCTCAGCTC

1601   GGACACCTTC TCTCCTCCCA GATTCCAGTA ACTCCCAATC TTCTCTCTGC

1651   AGAGCCCAAA TCTTGTGACA AAACTCACAC ATGCCCACCG TGCCCAGGTA

1701   AGCCAGCCCA GGCCTCGCCC TCCAGCTCAA GGCGGGACAG GTGCCCTAGA

1751   GTAGCCTGCA TCCAGGACA GGCCCCAGCC GGGTGCTGAC ACGTCCACCT

1801   CCATCTCTTC CTCAGCACCT GAACTCCTGG GGGGACCGTC AGTCTTCCTC

1851   TTCCCCCCAA AACCCAAGGA CACCCTCATG ATCTCCCGGA CCCCTGAGGT

1901   CACATGCGTG GTGGTGGACG TGAGCCACGA AGACCCTGAG GTCAAGTTCA

1951   ACTGGTACGT GGACGGCGTG GAGGTGCATA ATGCCAAGAC AAAGCCGCGG

2001   GAGGAGCAGT ACAACAGCAC GTACCGGGTG GTCAGCGTCC TCACCGTCCT

2051   GCACCAGGAC TGGCTGAATG GCAAGGAGTA CAAGTGCAAG GTCTCCAACA

2101   AAGCCCTCCC AGCCCCCATC GAGAAAACCA TCTCCAAAGC CAAAGGTGGG

2151   ACCCGTGGGG TGCGAGGGCC ACATGGACAG AGGCCGGCTC GGCCCACCCT

2201   CTGCCCTGAG AGTGACCGCT GTACCAACCT CTGTCCTACA GGGCAGCCCC

2251   GAGAACCACA GGTGTACACC CTGCCCCCAT CCCGGGATGA GCTGACCAAG

2301   AACCAGGTCA GCCTGACCTG CCTGGTCAAA GGCTTCTATC CCAGCGACAT

2351   CGCCGTGGAG TGGGAGAGCA ATGGGCAGCC GGAGAACAAC TACAAGACCA

2401   CGCCTCCCGT GCTGGACTCC GACGGCTCCT TCTTCCTCTA CAGCAAGCTC

2451   ACCGTGGACA AGAGCAGGTG GCAGCAGGGG AACGTCTTCT CATGCTCCGT

2501   GATGCATGAG GCTCTGCACA ACCACTACAC GCAGAAGAGC CTCTCCCTGT

2551   CTCCGGGTAA ATGAGTGCGA CGGCCGGCAA GCCCCGCTCC CCGGGCTCTC

2601   GCGGTCGCAC GAGGATGCTT GGCACGTACC CCCTGTACAT ACTTCCCGGG

2651   CGCCCAGCAT GGAAATAAAG CACCCAGCGC TGCCCTGGGC CCCTGCGAGA

2701   CTGTGATGGT TCTTTCCACG GGTCAGGCCG AGTCTGAGGC CTGAGTGGCA

2751   TGAGGGAGGC AGAGCGGGTC
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SEQ ID NO:30

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  1  MGWSCIILFL VATATGVHSA MHVAQPAVVL ASSRGIASFV CEYASPGKAT

 51  EVRVTVLRQA DSQVTEVCAA TYMMGNELTF LDDSICTGTS SGNQVNLTIQ

101  GLRAMDTGLY ICKVELMYPP PYYLGIGNGA QITVAAPSVF IFPPSDEQLK

151  SGTASVVCLL NNFYPREAKV QWKVDNALQS GNSQESVTEQ DSKDSTYSLS

201  STLTLSKADY EKHKVYACEV THQGLSSPVT KSFNRGEC*
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SEQ ID NO: 31

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  1  CATTCGCTTA CCTCGAGAAG CTTGAGATCA CAGTTCTCTC TACAGTTACT

 51  GAGCACACAG GACCTCACCA TGGGATGGAG CTGTATCATC CTCTTCTTGG

101  TAGCAACAGC TACAGGTAAG GGGCTCACAG TAGCAGGCTT GAGGTCTGGA

151  CATATATATG GGTGACAATG ACATCCACTT TGCCTTTCTC TCCACAGGTG

201  TCCACTCCGC AATGCACGTG GCCCAGCCTG CTGTGGTACT GGCCAGCAGC

251  CGAGGCATCG CCAGCTTTGT GTGTGAGTAT GCATCTCCAG GCAAAGCCAC

301  TGAGGTCCGG GTGACAGTGC TTCGGCAGGC TGACAGCCAG GTGACTGAAG

351  TCTGTGCGGC AACCTACATG ATGGGGAATG AGTTGACCTT CCTAGATGAT

401  TCCATCTGCA CGGGCACCTC CAGTGGAAAT CAAGTGAACC TCACTATCCA

451  AGGACTGAGG GCCATGGACA CGGGACTCTA CATCTGCAAG GTGGAGCTCA

501  TGTACCCACC GCCATACTAC CTGGGCATAG GCAACGGAGC CCAGATTAAA

551  CGTGAGTAGA ATTTAAACTT TGCTTCCTCA GTTTCTAGAA GAATGGCTGC

601  AAAGAGCTCC AACAAACAA TTTAGAACTT TATTAAGGAA TAGGGGGAAG

651  CTAGGAAGAA ACTCAAAACA TCAAGATTTT AAATACGCTT CTTGGTCTCC

701  TTGCTATAAT TATCTGGGAT AAGCATGCTG TTTTCTGTCT GTCCCTAACA

751  TGCCCTGTGA TTATCCGCAA ACAACACACC CAAGGGCAGA ACTTTGTTAC

801  TTAAACACCA TCCTGTTTGC TTCTTTCCTC AGGAACTGTG GCTGCACCAT

851  CTGTCTTCAT CTTCCCGCCA TCTGATGAGC AGTTGAAATC TGGAACTGCC

901  TCTGTTGTGT GCCTGCTGAA TAACTTCTAT CCCAGAGAGG CCAAAGTACA

951  GTGGAAGGTG GATAACGCCC TCCAATCGGG TAACTCCCAG GAGAGTGTCA
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1001   CAGAGCAGGA  CAGCAAGGAC  AGCACCTACA  GCCTCAGCAG  CACCCTGACG

1051   CTGAGCAAAG  CAGACTACGA  GAAACACAAA  GTCTACGCCT  GCGAAGTCAC

1101   CCATCAGGGC  CTGAGCTCGC  CCGTCACAAA  GAGCTTCAAC  AGGGGAGAGT

1151   GTTAGAGGGA  GAAGTGCCCC  CACCTGCTCC  TCAGTTCCAG  CCTGACCCCC

1201   TCCCATCCTT  TGGCCTCTGA  CCCTTTTTCC  ACAGGGGACC  TACCCCTATT

1251   GCGGTCCTCC  AGCTCATCTT  TCACCTCACC  CCCCTCCTCC  TCCTTGGCTT

1301   TAATTATGCT  AATGTTGGAG  GAGAATGAAT  AAATAAAGTG  AATCTTTGCA

1351   CCTGTGGTTT  CTCTCTTTCC  TCAATTAAT  AATTATTATC  TGTTGTTTAC

1401   CAACTACTCA  ATTTCTCTTA  TAAGGGACTA  AATATGTAGT  CATCCTAAGG

1451   CGCATAACCA  TTTATAAAAA  TCATCCTTCA  TTCTATTTTA  CCCTATCATC

1501   CTCTGCAAGA  CAGTCCTCCC  TCAAACCCAC  AAGCCTTCTG  TCCTCACAGT

1551   CCCCTGGGCC  GTGGTAGGAG  AGACTTGCTT  CCTTGTTTTC  CCCTCCTCAG

1601   CAAGCCCTCA  TAGTCCTTTT  TAAGGGTGAC  AGGTCTTACG  GTCATATATC

1651   CTTTGATTCA  ATTCCCTGGG  AATCAACCAA  GGCAAATTTT  TCAAAAGAAG

1701   AAACCTGC
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SEQ ID NO:32

```
  1   MGWSCIILFL  VATATGVHSA  MHVAQPAVVL  ASSRGIASFV  CEYASPGKAT

 51   EVRVTVLRQA  DSQVTEVCAA  TYMMGNELTF  LDDSICTGTS  SGNQVNLTIQ

101   GLRAMDTGLY  ICKVELMYPP  PYYLGIGNGA  QITVAAPSVF  IFPPSDEQLK

151   SGTASVVCLL  NNFYPREAKV  QWKVDNALQS  GNSQESVTEQ  DSKDSTYSLS

201   STLTLSKADY  EKHKVYACEV  THQGLSSPVT  KSFNRGEC*
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